

*Schulzer*

CRF Errors Corrected by the STIC System Branch

1632

Serial Number: 08/973,363

CRF Processing Date: 11/18/2000  
Edited by: AK  
Verified by: AK (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☒ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: moved (IV) CORRESP. ADDRESS: section up a few lines

**ENTERED**

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
TIME: 14:03:25

INPUT SET: S34486.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4 (i) APPLICANT:  
5 (A) NAME: GRIFFITHS, RICHARD  
6 (B) STREET: 20 (TR) Woodcroft Avenue, Broomhill,  
7 (C) CITY: Glasgow  
8 (E) COUNTRY: United Kingdom  
9 (F) POSTAL CODE (ZIP): G11 7HX  
10  
11 (A) NAME: TIWARI, BELA  
12 (B) STREET: 4 Upway Road  
13 (C) CITY: Oxford  
14 (E) COUNTRY: United Kingdom  
15 (F) POSTAL CODE (ZIP): OX3 9QH  
16 (ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR  
17 SEX IDENTIFICATION IN BIRDS  
18 (iii) NUMBER OF SEQUENCES: 39  
19 (iv) CORRESPONDENCE ADDRESS:  
20 (A) ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.  
21 (B) STREET: 2033 K. Street, N.W., Suite 800,  
22 (C) CITY: Washington  
23 (D) STATE: D.C.  
24 (E) COUNTRY: U.S.A.  
25 (F) ZIP: 20006  
26 (v) COMPUTER READABLE FORM:  
27 (A) MEDIUM TYPE: Floppy disk  
28 (B) COMPUTER: IBM PC compatible  
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
31 (vi) CURRENT APPLICATION DATA:  
32 (A) APPLICATION NUMBER:  
33 (B) FILING DATE:  
34 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: WO PCT/GB96/01341  
36 (B) FILING DATE: 05-JUN-1996  
37 (vii) PRIOR APPLICATION DATA:  
38 (A) APPLICATION NUMBER: GB 9511439.3  
39 (B) FILING DATE: 06-JUN-1995  
40 (viii) ATTORNEY/AGENT INFORMATION:  
41 (A) NAME: Warren M Cheek, Jr.  
42 (B) REGISTRATION NUMBER: 33,367  
43 (C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: (202)-721-8200  
46 (B) TELEFAX: (202)-721-8250

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PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
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47 (C) TELEX:  
48 (2) INFORMATION FOR SEQ ID NO: 1:  
49 (i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 723 base pairs  
51 (B) TYPE: nucleic acid  
52 (C) STRANDEDNESS: double  
53 (D) TOPOLOGY: linear  
54 (ii) MOLECULE TYPE: DNA (genomic)  
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
56 CCCGGTCGGA GGTTC AAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC 60  
57 AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT 120  
58 AATTCATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTGA GCGAAGTTTG TTGGGGGATT 180  
59 TTAGTTTGGT TTCCCTGTCA CTGTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG 240  
60 AGAATTGCTG TATTTGTGAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA 300  
61 CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG 360  
62 ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC 420  
63 ATTAATTGCT TGTTTTATGA AACCACCTCT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA 480  
64 TATCCTGTGG TAATGAGTTA ATGCATTAG AAGCACATGG CAGAACTAGG AGATCTGTGG 540  
65 ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT 600  
66 CTGAGGCTAG TTTCTTGAGC TGAAGTAAA TTTTGTGAGA ATATTTTCAA GACTACATTA 660  
67 GTTGTGTGTT TGAGGAAAAA TAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC 720  
68 GGG 723  
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70 (2) INFORMATION FOR SEQ ID NO: 2:  
71 (i) SEQUENCE CHARACTERISTICS:  
72 (A) LENGTH: 153 base pairs  
73 (B) TYPE: nucleic acid  
74 (C) STRANDEDNESS: double  
75 (D) TOPOLOGY: linear  
76 (ii) MOLECULE TYPE: cDNA  
77  
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
79 ATTCTTCAG ATGATCCTGA TAAAAACCA CAAGCAAAC AGTTACAGAC CAAAAACCA 60  
80 CAAGCAAAC AGTTACAGAC CCGTGAGAC TACCTCATCA AACTACTTAG CAGAGATCTT 120  
81 GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG 153  
82  
83 (2) INFORMATION FOR SEQ ID NO: 3:  
84 (i) SEQUENCE CHARACTERISTICS:  
85 (A) LENGTH: 153 base pairs  
86 (B) TYPE: nucleic acid  
87 (C) STRANDEDNESS: double  
88 (D) TOPOLOGY: linear  
89 (ii) MOLECULE TYPE: cDNA  
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
91 ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC 60  
92 CAGGCAAAGC AGCTACAGAC CCGTGAGAC TACCTCATTA AATTACTGAA TAAAGACCTT 120  
93 GCAAGAAAGG AAGCACAAG GCTTGCTGGT GCA 153  
94 (2) INFORMATION FOR SEQ ID NO: 4:  
95  
96 (i) SEQUENCE CHARACTERISTICS:  
97 (A) LENGTH: 153 base pairs  
98 (B) TYPE: nucleic acid  
99 (C) STRANDEDNESS: double

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PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
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100 (D) TOPOLOGY: linear  
101 (ii) MOLECULE TYPE: cDNA  
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
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104 ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC 60  
105 CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATT AATTACTGAA TAAAGACCTT 120  
106 GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA 153  
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108 (2) INFORMATION FOR SEQ ID NO: 5:  
109 (i) SEQUENCE CHARACTERISTICS:  
110 (A) LENGTH: 153 base pairs  
111 (B) TYPE: nucleic acid  
112 (C) STRANDEDNESS: double  
113 (D) TOPOLOGY: linear  
114 (ii) MOLECULE TYPE: cDNA  
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
116 ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA 60  
117 CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATT AATTACTGAA TAAAGACCTT 120  
118 GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA 153  
119  
120 (2) INFORMATION FOR SEQ ID NO: 6:  
121 (i) SEQUENCE CHARACTERISTICS:  
122 (A) LENGTH: 41 amino acids  
123 (B) TYPE: amino acid  
124 (C) STRANDEDNESS:  
125 (D) TOPOLOGY: linear  
126 (ii) MOLECULE TYPE: peptide  
127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
128 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
129 1 5 10 15  
130 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys  
131 20 25 30  
132 Arg Glu Ala Gln Arg Leu Cys Gly Ala  
133 35 40  
134  
135 (2) INFORMATION FOR SEQ ID NO: 7:  
136 (i) SEQUENCE CHARACTERISTICS:  
137 (A) LENGTH: 41 amino acids  
138 (B) TYPE: amino acid  
139 (C) STRANDEDNESS:  
140 (D) TOPOLOGY: linear  
141 (ii) MOLECULE TYPE: peptide  
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
143 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
144 1 5 10 15  
145 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
146 20 25 30  
147 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
148 35 40  
149  
150 (2) INFORMATION FOR SEQ ID NO: 8:  
151 (i) SEQUENCE CHARACTERISTICS:  
152 (A) LENGTH: 41 amino acids

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PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
TIME: 14:03:26

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153 (B) TYPE: amino acid  
154 (C) STRANDEDNESS:  
155 (D) TOPOLOGY: linear  
156 (ii) MOLECULE TYPE: peptide  
157 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
158 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
159 1 5 10 15  
160 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
161 20 25 30  
162 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
163 35 40  
164  
165 (2) INFORMATION FOR SEQ ID NO: 9:  
166 (i) SEQUENCE CHARACTERISTICS:  
167 (A) LENGTH: 41 amino acids  
168 (B) TYPE: amino acid  
169 (C) STRANDEDNESS:  
170 (D) TOPOLOGY: linear  
171 (ii) MOLECULE TYPE: peptide  
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
173 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
174 1 5 10 15  
175 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
176 20 25 30  
177 Lys Glu Val Gln Arg Leu Thr Gly Ala  
178 35 40  
179  
180 (2) INFORMATION FOR SEQ ID NO: 10:  
181 (i) SEQUENCE CHARACTERISTICS:  
182 (A) LENGTH: 6608 base pairs  
183 (B) TYPE: nucleic acid  
184 (C) STRANDEDNESS: double  
185 (D) TOPOLOGY: linear  
186 (ii) MOLECULE TYPE: cDNA  
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
188 CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCCTGGC 60  
189 CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG 120  
190 CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC 180  
191 ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA 240  
192 GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG 300  
193 GGTGAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA 360  
194 GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG 420  
195 AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT 480  
196 CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA 540  
197 AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA 600  
198 GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAACTAA GAAGAAAAAG CATAAAGATG 660  
199 AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG 720  
200 CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGAATATGAG CCAAAAAACA 780  
201 AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG 840  
202 GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG 900  
203 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA 960  
204 CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG 1020  
205

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PATENT APPLICATION US/08/973,363DATE: 01/18/2000  
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206	AAGATGAATT	TGAACTATA	GAGAAGTTTA	TGGACAGTCG	AATTGGCCGA	AAAGGAGCCA	1080
207	CTGGTGCCTC	AACCACCATC	TATGCCGTTG	AGGCAGATGG	TGACCCAAAT	GCTGGGTTTG	1140
208	AAAAGTCAAA	GGAGCTGGGA	GAAATACAGT	ATCTTATTAA	ATGGAAAGGC	TGGTCACACA	1200
209	TCCATAACAC	TTGGGAAACT	GAAGAAACGC	TGAAGCAACA	AAATGTTAAA	GGAATGAACA	1260
210	AACTGGACAA	CTACAAGAAA	AAGGATCAGG	AGACAAAACG	CTGGCTGAAA	AATGCTTCTC	1320
211	CAGAAGATGT	GGAATATTAT	AACTGCCAGC	AGGAGCTTAC	AGATGATCTG	CACAAACAAT	1380
212	ATCAAATAGT	GGAAAGAATA	ATTGCTCATT	CAAAATCAAAA	GTCAGCAGCT	GGTTATCCGG	1440
213	ACTACTATTG	CAAATGGCAG	GGTCTGCCTT	ACTCAGAATG	TAGCTGGGAA	GATGGTGTCT	1500
214	TCATTGCCAA	AAAGTTTCAG	GCACGCATTG	ATGAGTATTT	TAGCAGAAAT	CAATCCAAGA	1560
215	CTACTCCCTT	TAAGGACTGC	AAGGTTCTAA	AACAGAGACC	AAGATTTGTT	GCACTGAAGA	1620
216	AGCAACCATC	TTACATTGGA	GGACATGAAA	GTCTGGAGTT	AAGAGATTAT	CAGTTAAATG	1680
217	GATTGAATTG	GCTCGCTCAT	TCATGGTGCA	AAGGAAATAG	TTGTATTCTT	GCAGATGAAA	1740
218	TGGGTCTGGG	TAAACAATA	CAAACAATTT	CTTTTCTGAA	CTACCTGTTT	CATGAACATC	1800
219	AACTGTATGG	CCCTTTTCTT	CTGCGCGTGC	CACCTTCTAC	CTTGACATCT	TGGCAAAGAG	1860
220	AGATTCAAAC	TTGGGCTCCT	CAGATGAATG	CTGTAGTTTA	CTTAGGAGAT	ATAACTAGTA	1920
221	GAAATATGAT	AAGGACTCAT	GAATGGATGC	ATCCACAGAC	TAAACGATTA	AAGTTTAAAC	1980
222	TACTTCTGAC	GACATATGAA	ATTTTACTGA	AGGATAAGTC	ATTCTTGGT	GGTCTCAATT	2040
223	GGGCATTCAT	AGGAGTTGAT	GAAGCTCATC	GTTTAAAAAA	TGATGACTCT	CTTCTGTACA	2100
224	GGACTTTAAT	AGACTTTAAG	TCCAACCATC	GACTTCTGAT	TACTGGAACC	CCACTGCAAA	2160
225	ATTCCTCAA	AGAGCTGTGG	TCTTTGTTGC	ATTTTCATCAT	GCCAGAAAAA	TTTTCTCTCT	2220
226	GGGAAGATTT	TGAAGAGGAG	CATGCGAAAG	GAAGAGAGTA	TGGTTATGCA	AGTCTTCACA	2280
227	AAGAGCTTGA	ACCATTTTGA	CTAAGAAGAG	TTAAAAAAGA	TGTAGAAAAG	TCTTTACCTG	2340
228	CTAAGGTTGA	ACAAATCTG	AGGATGGAAA	TGAGTGCATT	GCAGAAGCAA	TATTACAAGT	2400
229	GGATTTTAAC	AAGGAATTAT	AAAGCCCTCA	GTAAAGGTTT	AAAAGGCAGT	ACCTCAGGCT	2460
230	TTCTGAACAT	TATGATGGAA	CTTAAGAAGT	GTTGTAACCA	TTGCTACCTC	ATTAAGCCAC	2520
231							
232	CAGATGATAA	TGAATTCTAT	AATAAACAGG	AGGCCTTACA	GCATTTGATA	CGTAGCAGCG	2580
233	GGAAACTAAT	CCTTCTTGAC	AAGCTACTGA	TTCGTCTGCG	AGAACGTGGC	AACAGAGTTC	2640
234	TGATTTTCTC	TCAGATGGTG	AGGATGCTGG	ACATCCTAGC	AGAATATCTG	AAGTATCGCC	2700
235	AGTTTCCCTT	CCAGAGACTT	GATGGATCAA	TAAAAGGGGA	ATTGAGGAAG	CAAGCACTGG	2760
236	ATCATTTCAA	TGCAGAAGGA	TCAGAGGATT	TCTGTTTTTT	ACTGTCTACA	AGAGCTGGAG	2820
237	GATTAGGTAT	TAAGTTGGCA	TCTGCTGACA	CTGTAGTTAT	TTTTGATTCT	GACTGGAATC	2880
238	CACAGAATGA	TCTGCAGGCA	CAGGCGAGAG	CTCATAGAAT	TGGACAGAAG	AAACAGGTTA	2940
239	ATATTTATCG	GCTAGTCACA	AAAGGATCAG	TAGAAGAAGA	TATTCTTGAA	AGAGCCAAGA	3000
240	AGAAGATGGT	GCTAGACCAT	TTAGTAATTC	AGAGAATGGA	CACGACAGGA	AAAACGTGTC	3060
241	TGCATACAGG	TTCAACTCCA	TCAAGCTCTA	CACCTTTTAA	TAAAGAAGAG	TTATCAGCTA	3120
242	TTTTGAAGTT	TGGTGTGAG	GAACCTTTTA	AAGAACCTGA	AGGAGAAGAA	CAGGAGCCCC	3180
243	AGGAAATGGA	TATAGATGAA	ATCTTGAAGA	GAGCTGAAAC	TGGGAAAAT	GAGCCAGGTC	3240
244	CATTGACTGT	AGGGGATGAG	TTGCTTTCAC	AGTTCAAGGT	GGCGAACTTT	TCCAATATGG	3300
245	ATGAAGATGA	TATTGAGTTG	GAACCAGAAA	GAAATTCAG	AAATTGGGAA	GAAATCATCC	3360
246	CAGAATCCCA	ACGGAGAAGG	ATAGAGGAGG	AGGAAAGACA	AAAAGAACTT	GAAGAAATAT	3420
247	ACATGCTCCC	GAGGATGAGA	AACTGTGCAA	AACAGATCAG	CTTTAATGGG	AGTGAAGGAA	3480

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363DATE: 01/19/2000  
TIME: 01:34:47

INPUT SET: S34486.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

Does Not Comply  
Corrected Diskette Needed

1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4 (i) APPLICANT:  
5 (A) NAME: GRIFFITHS, RICHARD  
6 (B) STREET: 20 (TR) Woodcroft Avenue, Broomhill,  
7 (C) CITY: Glasgow  
8 (E) COUNTRY: United Kingdom  
9 (F) POSTAL CODE (ZIP): G11 7HX  
10  
11 (A) NAME: TIWARI, BELA  
12 (B) STREET: 4 Upway Road  
13 (C) CITY: Oxford  
14 (E) COUNTRY: United Kingdom  
15 (F) POSTAL CODE (ZIP): OX3 9QH  
16 (ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR  
17 SEX IDENTIFICATION IN BIRDS  
18 (iii) NUMBER OF SEQUENCES: 39  
19 (iv) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
24 (vi) ~~(vii)~~ CURRENT APPLICATION DATA: *add headings*  
25 (vii) ~~(viii)~~ PRIOR APPLICATION DATA:  
26 (A) APPLICATION NUMBER: WO PCT/GB96/01341  
27 (B) FILING DATE: 05-JUN-1996  
28 (viii) ~~(ix)~~ PRIOR APPLICATION DATA:  
29 (A) APPLICATION NUMBER: GB 9511439.3  
30 (B) FILING DATE: 06-JUN-1995  
31 (iv) ~~(v)~~ CORRESPONDENCE ADDRESS:  
32 (A) ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.  
33 (B) STREET: 2033 K. Street, N.W., Suite 800,  
34 (C) CITY: Washington  
35 (D) STATE: D.C.  
36 (E) COUNTRY: U.S.A.  
37 (F) ZIP: 20006  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Warren M Cheek, Jr.  
40 (B) REGISTRATION NUMBER: 33,367  
41 (C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: (202)-721-8200  
44 (B) TELEFAX: (202)-721-8250  
45 (C) TELEX:  
46 (2) INFORMATION FOR SEQ ID NO: 1:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,363DATE: 01/19/2000  
TIME: 01:34:48

INPUT SET: S34486.raw

47 (i) SEQUENCE CHARACTERISTICS:  
48 (A) LENGTH: 723 base pairs  
49 (B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: double  
51 (D) TOPOLOGY: linear  
52 (ii) MOLECULE TYPE: DNA (genomic)  
53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
54 CCCGGTCGGA GGTTTCAAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC 60  
55 AAGGTGATGG TTGGTCAAAA GTTGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT 120  
56 AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTGA GCGAAGTTTG TTTGGGGATT 180  
57 TTAGTTTGGT TTCCCTGTCA CTGTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG 240  
58 AGAATTGCTG TATTGTTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA 300  
59 CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG 360  
60 ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC 420  
61 ATTAATTGCT TGTTTTATGA AACCCTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA 480  
62 TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG 540  
63 ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT 600  
64 CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTGTGAGA ATATTTTCAA GACTACATTA 660  
65 GTTGTGTGTT TGAGGAAAAA TAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC 720  
66 GGG 723  
67  
68 (2) INFORMATION FOR SEQ ID NO: 2:  
69 (i) SEQUENCE CHARACTERISTICS:  
70 (A) LENGTH: 153 base pairs  
71 (B) TYPE: nucleic acid  
72 (C) STRANDEDNESS: double  
73 (D) TOPOLOGY: linear  
74 (ii) MOLECULE TYPE: cDNA  
75  
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
77 ATTCTTCAG ATGATCCTGA TAAAAACCA CAAGCAAAC AGTTACAGAC CAAAAACCA 60  
78 CAAGCAAAC AGTTACAGAC CCGTCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT 120  
79 GCAAAAAGAG AGGCTCAGAG ACTTGTGGT GCG 153  
80  
81 (2) INFORMATION FOR SEQ ID NO: 3:  
82 (i) SEQUENCE CHARACTERISTICS:  
83 (A) LENGTH: 153 base pairs  
84 (B) TYPE: nucleic acid  
85 (C) STRANDEDNESS: double  
86 (D) TOPOLOGY: linear  
87 (ii) MOLECULE TYPE: cDNA  
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
89 ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC 60  
90 CAGGCAAAGC AGCTACAGAC CCGTCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT 120  
91 GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA 153  
92 (2) INFORMATION FOR SEQ ID NO: 4:  
93  
94 (i) SEQUENCE CHARACTERISTICS:  
95 (A) LENGTH: 153 base pairs  
96 (B) TYPE: nucleic acid  
97 (C) STRANDEDNESS: double  
98 (D) TOPOLOGY: linear  
99 (ii) MOLECULE TYPE: cDNA



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100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
101  
102 ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC 60  
103 CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
104 GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA 153  
105  
106 (2) INFORMATION FOR SEQ ID NO: 5:  
107 (i) SEQUENCE CHARACTERISTICS:  
108 (A) LENGTH: 153 base pairs  
109 (B) TYPE: nucleic acid  
110 (C) STRANDEDNESS: double  
111 (D) TOPOLOGY: linear  
112 (ii) MOLECULE TYPE: cDNA  
113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
114 ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA 60  
115 CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
116 GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA 153  
117  
118 (2) INFORMATION FOR SEQ ID NO: 6:  
119 (i) SEQUENCE CHARACTERISTICS:  
120 (A) LENGTH: 41 amino acids  
121 (B) TYPE: amino acid  
122 (C) STRANDEDNESS:  
123 (D) TOPOLOGY: linear  
124 (ii) MOLECULE TYPE: peptide  
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
126 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
127 1 5 10 15  
128 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys  
129 20 25 30  
130 Arg Glu Ala Gln Arg Leu Cys Gly Ala  
131 35 40  
132  
133 (2) INFORMATION FOR SEQ ID NO: 7:  
134 (i) SEQUENCE CHARACTERISTICS:  
135 (A) LENGTH: 41 amino acids  
136 (B) TYPE: amino acid  
137 (C) STRANDEDNESS:  
138 (D) TOPOLOGY: linear  
139 (ii) MOLECULE TYPE: peptide  
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
141 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
142 1 5 10 15  
143 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
144 20 25 30  
145 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
146 35 40  
147  
148 (2) INFORMATION FOR SEQ ID NO: 8:  
149 (i) SEQUENCE CHARACTERISTICS:  
150 (A) LENGTH: 41 amino acids  
151 (B) TYPE: amino acid  
152 (C) STRANDEDNESS:

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153 (D) TOPOLOGY: linear  
154 (ii) MOLECULE TYPE: peptide  
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
156 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
157 1 5 10 15  
158 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
159 20 25 30  
160 Lys Glu Ala Gln Arg Leu Ala Gly Ala  
161 35 40  
162  
163 (2) INFORMATION FOR SEQ ID NO: 9:  
164 (i) SEQUENCE CHARACTERISTICS:  
165 (A) LENGTH: 41 amino acids  
166 (B) TYPE: amino acid  
167 (C) STRANDEDNESS:  
168 (D) TOPOLOGY: linear  
169 (ii) MOLECULE TYPE: peptide  
170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
171 Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
172 1 5 10 15  
173 Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
174 20 25 30  
175 Lys Glu Val Gln Arg Leu Thr Gly Ala  
176 35 40  
177  
178 (2) INFORMATION FOR SEQ ID NO: 10:  
179 (i) SEQUENCE CHARACTERISTICS:  
180 (A) LENGTH: 6608 base pairs  
181 (B) TYPE: nucleic acid  
182 (C) STRANDEDNESS: double  
183 (D) TOPOLOGY: linear  
184 (ii) MOLECULE TYPE: cDNA  
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
186 CCGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CCGGCCGGGG AAGGCCTGGC 60  
187 CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG 120  
188 CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC 180  
189 ACCTTGTAAC CTGAGTGGAC TTTCTTTTAA ACTTCTTAAT ACTTACAATG AATGGGCACA 240  
190 GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG 300  
191 GGTCAGCTTC AGGTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA 360  
192 GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG 420  
193 AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT 480  
194 CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA 540  
195 AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA 600  
196 GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAACTAA GAAGAAAAAG CATAAAGATG 660  
197 AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG 720  
198 CGGAAGATGG GGATAAAGC AGTTGTGAAG AAAGTGAATC TGAATATGAG CCAAAAAACA 780  
199 AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG 840  
200 GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG 900  
201 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA 960  
202 CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG 1020  
203  
204 AAGATGAATT TGAAACTATA GAGAAGTTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA 1080  
205 CTGGTGCCCTC AACCACCATC TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG 1140

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206	AAAAGTCAAA	GGAGCTGGGA	GAAATACAGT	ATCTTATTAA	ATGGAAAGGC	TGGTCACACA	1200
207	TCCATAACAC	TTGGGAAACT	GAAGAAACGC	TGAAGCAACA	AAATGTTAAA	GGAATGAACA	1260
208	AACTGGACAA	CTACAAGAAA	AAGGATCAGG	AGACAAAACG	CTGGCTGAAA	AATGCTTCTC	1320
209	CAGAAGATGT	GGAATATTAT	AACTGCCAGC	AGGAGCTTAC	AGATGATCTG	CACAAACAAT	1380
210	ATCAAATAGT	GGAAAGAATA	ATTGCTCATT	CAAATCAAAA	GTCAGCAGCT	GGTTATCCGG	1440
211	ACTACTATTG	CAAATGGCAG	GGTCTGCCTT	ACTCAGAATG	TAGCTGGGAA	GATGGTGCTC	1500
212	TCATTGCCAA	AAAGTTTCAG	GCACGCATTG	ATGAGTATTT	TAGCAGAAAT	CAATCCAAGA	1560
213	CTACTCCCTT	TAAGGACTGC	AAGTTCTTAA	AACAGAGACC	AAGATTTGTT	GCACTGAAGA	1620
214	AGCAACCATC	TTACATTGGA	GGACATGAAA	GTCTGGAGTT	AAGAGATTAT	CAGTTAAATG	1680
215	GATTGAATTG	GCTCGCTCAT	TCATGGTGCA	AAGGAAATAG	TTGTATTCTT	GCAGATGAAA	1740
216	TGGGTCTGGG	TAAAACAATA	CAACAATTT	CTTTTCTGAA	CTACCTGTTT	CATGAACATC	1800
217	AACGTATATG	CCCTTTTCTT	CTGCGCGTGC	CACTTTCTAC	CTTGACATCT	TGGCAAAGAG	1860
218	AGATTCAAAC	TTGGGCTCCT	CAGATGAATG	CTGTAGTTTA	CTTAGGAGAT	ATAACTAGTA	1920
219	GAAATATGAT	AAGGACTCAT	GAATGGATGC	ATCCACAGAC	TAAACGATTA	AAGTTTAAAC	1980
220	TACTTCTGAC	GACATATGAA	ATTTTACTGA	AGGATAAGTC	ATTCCTTGGT	GGTCTCAATT	2040
221	GGGCATT CAT	AGGAGTTGAT	GAAGCTCATC	GTTTAAAAAA	TGATGACTCT	CTTCTGTACA	2100
222	GGACTTTAAT	AGACTTTAAG	TCCAACCATC	GACTTCTGAT	TACTGGAACC	CCACTGCAAA	2160
223	ATTCCTCAA	AGAGCTGTGG	TCTTTGTTGC	ATTTCAATCAT	GCCAGAAAAA	TTTTCTCTCT	2220
224	GGGAAGATTT	TGAAGAGGAG	CATGGCAAAG	GAAGAGAGTA	TGGTTATGCA	AGTCTTCACA	2280
225	AAGAGCTTGA	ACCATTTTTA	CTAAGAAGAG	TTAAAAAAGA	TGTAGAAAAG	TCTTTACCTG	2340
226	CTAAGGTTGA	ACAAATTCTG	AGGATGGAAA	TGAGTGCATT	GCAGAAGCAA	TATTACAAGT	2400
227	GGATTTTAAC	AAGGAATTAT	AAAGCCCTCA	GTAAAGGTTT	AAAAGGCAGT	ACCTCAGGCT	2460
228	TTCTGAACAT	TATGATGGAA	CTTAAGAAGT	GTTGTAACCA	TTGCTACCTC	ATTAAGCCAC	2520
229							
230	CAGATGATAA	TGAATTCTAT	AATAAACAGG	AGGCCTTACA	GCATTTGATA	CGTAGCAGCG	2580
231	GGAAACTAAT	CCTTCTTGAC	AAGCTACTGA	TTCGTCTGCG	AGAACGTGGC	AACAGAGTTC	2640
232	TGATTTTCTC	TCAGATGGTG	AGGATGCTGG	ACATCCTAGC	AGAATATCTG	AAGTATCGCC	2700
233	AGTTTCCCTT	CCAGAGACTT	GATGGATCAA	TAAAAGGGGA	ATTGAGGAAG	CAAGCACTGG	2760
234	ATCATTTCAA	TGCAGAAGGA	TCAGAGGATT	TCTGTTTTTT	ACTGTCTACA	AGAGCTGGAG	2820
235	GATTAGGTAT	TAACTTGGCA	TCTGCTGACA	CTGTAGTTAT	TTTGTATTCT	GACTGGAATC	2880
236	CACAGAATGA	TCTGCAGGCA	CAGCGGAGAG	CTCATAGAAT	TGGACAGAAG	AAACAGGTTA	2940
237	ATATTTATCG	GCTAGTCACA	AAAGGATCAG	TAGAAGAAGA	TATTCTTGAA	AGAGCCAAGA	3000
238	AGAAGATGGT	GCTAGACCAT	TTAGTAATTC	AGAGAATGGA	CACGACAGGA	AAAAGTGTTC	3060
239	TGCATACAGG	TTCAACTCCA	TCAAGCTCTA	CACCTTTTTAA	TAAAGAAGAG	TTATCAGCTA	3120
240	TTTTGAAGTT	TGGTGCTGAG	GAAGCTTTTA	AAGAACCTGA	AGGAGAAGAA	CAGGAGCCCC	3180
241	AGGAAATGGA	TATAGATGAA	ATCTTGAAGA	GAGCTGAAAC	TCGGGAAAAA	GAGCCAGGTC	3240
242	CATTGACTGT	AGGGGATGAG	TTGCTTTTAC	AGTTCAAGGT	GGCGAACTTT	TCCAATATGG	3300
243	ATGAAGATGA	TATTGAGTTG	GAACCAGAAA	GAAATTC AAG	AAATTGGGAA	GAAATCATCC	3360
244	CAGAATCCCA	ACGGAGAAGG	ATAGAGGAGG	AGGAAAGACA	AAAAGAAGTT	GAAGAAATAT	3420
245	ACATGCTCCC	GAGGATGAGA	AACTGTGCAA	AACAGATCAG	CTTTAATGGG	AGTGAAGGAA	3480
246	GACGCAGTAG	GAGCAGAAGA	TATTCTGGAT	CTGATAGTGA	CTCCATCACA	GAAAGAAAAC	3540
247	GGCCAAAAAA	GCGTGGAAGA	CCTCGAACCA	TTCCTCGAGA	AAATATTAAA	GGATTTAGTG	3600
248	ATGCAGAGAT	CAGGCGGTTT	ATCAAGAGTT	ACAAGAAATT	TGGTGGCCCT	CTGGAAAAGT	3660
249	TAGATGCTGT	AGCTAGAGAT	GCTGAACTGG	TTGATAAATC	TGAGACAGAC	CTTAGACGTT	3720
250	TGGGTGAACT	TGTACATAAT	GGATGCATTA	AGGCTTTAAA	GGACAATTCA	TCTGGACAAG	3780
251	AAAGAGCAGG	AGGTAGACTT	GGGAAAGTTA	AAGGCCCAAC	GTTTCGAATC	TCAGGAGTGC	3840
252	AGGTGAATGC	AAAAGTAGTC	ATCTCTCACG	AAGAAGAGCT	GGCACCCTG	CACAAATCCA	3900
253	TTCCCTTCAGA	TCCAGAAGAA	AGGAAAAGAT	ATGTCATCCC	ATGCCACACC	AAGGCTGCTC	3960
254	ACTTCGATAT	AGATTGGGGT	AAAGAAGATG	ATTCCAATCT	GTTAGTAGGC	ATCTATGAAT	4020
255							
256	ATGGCTATGG	CAGCTGGGAA	ATGATAAAAA	TGGATCCAGA	TCTCAGCTTA	ACACAGAAGA	4080
257	TTTTACCTGA	TGATCCAGAC	AAGAAACCCC	AGGCAAAGCA	GCTACAGACC	CGTGCAGACT	4140
258	ACCTCATTA	ATTACTGAAT	AAAGACCTTG	CAAGAAAGGA	AGCACAAGG	CTTGCTGCTG	4200

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CURRENT APPLICATION DATA